

## Amino Acids

Protein Alignment Summary Table (**Vpx**)

Name(s)	Accession No.	Region	First Author	Reference
ROD	M15390	complete genome	Guyader M	<i>Nature</i> <b>326</b> (6114), 662–669 (1987)
NIHZ	J03654	complete genome	Zagury JF	<i>PNAS</i> <b>85</b> 5941–5945 (1988)
ISY	J04498	complete genome	Franchini G	<i>PNAS</i> <b>86</b> 2433–2437 (1989)
ST	M31113	complete genome	Kumar P	<i>J Virol</i> <b>64</b> 890–901 (1990)
BEN	M30502	complete genome	Kirchhoff F	<i>Virology</i> <b>177</b> 305–311 (1990)
CAM2	D00835	complete genome	Tristem MF	<i>J Gen Virol</i> <b>72</b> 721 (1991)
D194	J04542	complete genome	Kuehnel H	<i>PNAS</i> <b>86</b> 2383–2387 (1989)
GHI	M30895	complete genome	Hasegawa A	<i>ARHR</i> <b>5</b> 593–604 (1989)
KR	U22047	complete genome	Kraus GK	<i>PNAS</i> <b>90</b> (9), 4226–4230 (1993)
MDS	Z48731	gag, pol, vif, tat, rev, nef, env	Becker M	Unpublished (1995)
UC2	U38293	complete genome	Barnett SW	Unpublished (1997)
UC1	L07625	complete genome	Barnett SW	<i>J Virol</i> <b>67</b> 1006–1014, (1993)
D205	X61240	complete genome	Dietrich U	<i>ARHR</i> <b>8</b> 1619 (1992)
EHOA	U27200	complete genome	Rey-Cuille MA	<i>Virology</i> <b>202</b> (1), 471–476 (1994)
DEC 98				
MM251	M19499	complete genome	Franchini G	<i>Nature</i> <b>328</b> 539–543 (1987)
MM1A11	M76764	complete genome	Luciw PA	<i>ARHR</i> <b>8</b> 395–402 (1992)
MM32H	D01065	complete genome	Rud EW	<i>J Gen Virol</i> <b>75</b> 529 (1994)
MM316S	L22790	vif, vpx, vpr	Kodama T	<i>J Virol</i> <b>67</b> 6522–6534 (1993)
MM239	M33262	complete genome	Regier DA	<i>ARHR</i> <b>6</b> 1221–1231 (1990)
MM142	M16403	complete genome	Chakrabarti L	<i>Nature</i> <b>328</b> 543–547 (1987)
MNE	M32741	complete genome	Benveniste RE	Unpublished (1990)
SMMPB14.441A	M31325	complete genome	Dewhurst S	<i>Nature</i> <b>345</b> 636–640 (1990)
SMMH9	M80194	complete genome	Courgaud V	<i>J Virol</i> <b>66</b> 414–419 (1992)
SMMH4	X14307	complete genome	Hirsch VM	<i>Nature</i> <b>339</b> 389–391 (1989)
SM62A	U04982	partial env, nef, tat, rev	Hirsch VM	<i>J Virol</i> <b>68</b> 2649–2661 (1994)
STM	M83293	complete genome	Novembre FJ	<i>Virology</i> <b>186</b> 783–787 (1992)

< vif cds

CONSENSUS-A	MtdPretvPPGNGSgPeTlqeAF?WldrvEAInREAVHlPRELIFQWQRsWryMdeqns?SYTKYRylchlnQkA?fiH?kkgcGtGggghPgg?W?Rp?GPPPPIPGLV	108
A_ROD	-A--N-----A-----A-----E-----A-----D-----H-----T-----T-----I-----I-----V-----V-----M-----M-----S-----S-----	113
A_NTHZ	-N-----I-----E-----E-----D-----D-----D-----H-----T-----T-----I-----I-----V-----V-----M-----M-----S-----S-----	112
A_IST	-A-----I-----E-----E-----D-----D-----D-----H-----T-----T-----I-----I-----V-----V-----M-----M-----S-----S-----	113
A_ST	-AG-----I-----E-----E-----D-----D-----D-----H-----T-----T-----I-----I-----V-----V-----M-----M-----S-----S-----	113
A_BEN	-A-----R-----E-----E-----I-----I-----I-----H-----T-----T-----I-----I-----V-----V-----P-----P-----#-----#-----	113
A_CAM2	-A-----R-----E-----E-----I-----I-----I-----H-----T-----T-----I-----I-----V-----V-----P-----P-----#-----#-----	113
A_DJ194	-A-----R-----E-----E-----I-----I-----I-----H-----T-----T-----I-----I-----V-----V-----P-----P-----#-----#-----	113
A_GHL	-A-----R-----E-----E-----I-----I-----I-----H-----T-----T-----I-----I-----V-----V-----P-----P-----#-----#-----	113
A_KR	-A-----K-----G-----V-----A-----E-----M-----D-----P-----D-----P-----D-----P-----R-----Y-----M-----V-----	111
A_MDS	-A-----K-----G-----V-----A-----E-----M-----D-----Q-----D-----Q-----D-----Q-----R-----Y-----M-----V-----	111
A_UC2	-A-----K-----G-----V-----A-----E-----M-----D-----Q-----D-----Q-----D-----Q-----R-----Y-----M-----V-----	112
CONSENSUS-B	R-----R-----d-----v-----E-----i-----tel-----V-----A-----R-----E-----I-----I-----L-----M-----V-----Y-----T-----#-----	110
B_UC1	.----R-----R-----D-----D-----E-----i-----tel-----V-----C-----A-----R-----E-----I-----I-----L-----M-----V-----Y-----T-----#-----	112
B_D205	.----R-----R-----D-----D-----V-----A-----E-----i-----tel-----V-----A-----R-----E-----I-----I-----L-----M-----V-----Y-----T-----#-----	112
B_EHOA	.----R-----R-----D-----D-----V-----A-----E-----i-----tel-----V-----A-----R-----E-----I-----I-----L-----M-----V-----Y-----T-----#-----	111
CONSENSUS-SD	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----Q-----V-----L-----M-----C-----R-----E-----A-----	111
SD_MM251	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----Q-----V-----L-----M-----C-----R-----E-----A-----	113
SD_MM1A1	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----P-----V-----I-----L-----M-----C-----R-----E-----A-----	113
SD_MM32H	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----P-----V-----I-----L-----M-----C-----R-----E-----A-----	113
SD_MM316S	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----P-----V-----I-----L-----M-----C-----R-----E-----A-----	112
SD_MM239	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----P-----V-----I-----L-----M-----C-----R-----E-----A-----	113
SD_MM142	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----P-----V-----I-----L-----M-----C-----R-----E-----A-----	113
SD_MNE	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----O-----V-----I-----L-----M-----C-----R-----E-----A-----	113
SD_SNMPB14_441_A	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----O-----V-----I-----L-----M-----C-----R-----E-----A-----	112
SD_SNMPB14_441_B	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----O-----V-----I-----M-----M-----C-----R-----E-----A-----	112
SD_SNMPB14_5_S	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----O-----V-----I-----M-----M-----C-----R-----E-----A-----	112
SD_SNMPB14_6	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----O-----V-----I-----M-----M-----C-----R-----E-----A-----	112
SD_SNMPH9	xx-----xi-----xx-----x-----D-----H-----x-----E-----A-----x-----R-----x-----E-----M-----V-----x-----I-----L-----M-----C-----R-----E-----A-----	113
SD_SNMPH4	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----T-----	113
SD_SN62A	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----T-----	91
CONSENSUS-STM	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----A-----	113
STM_STM	S-----R-----I-----I-----V-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----E-----A-----	113